GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 18, 2002, 04:48:39 ; Search time 42.56 Seconds
(without alignments)
327.515 Million cell updates/sec

Title: US-09-719-748-2
Perfect score: 1846
Sequence: 1 MEPFKQQKVEDFYDIGEELG.....TEEDIARRKALHPRRRSSTS 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1293	70.0	1431	1	DAPK_HUMAN	P53355 homo sapien
2	703.5	38.1	1176	1	KMLS_BOVIN	Q28824 bos taurus
3	698	37.8	1914	1	KMLS_HUMAN	Q15746 homo sapien
4	694	37.6	1147	1	KMLS_RABIT	P29294 oryctolagus
5	685.5	37.1	1906	1	KMLS_CHICK	P11799 gallus gall
6	668.5	36.2	414	1	S17A_HUMAN	Q9uee5 homo sapien
7	659.5	35.7	397	1	S17A_RABIT	Q9gm70 oryctolagus
8	641.5	34.8	372	1	S17B_HUMAN	O94768 homo sapien
9	637	34.5	438	1	KMLS_SHEEP	O02827 ovis aries
10	605	32.8	607	1	KMLC_RABIT	P07313 oryctolagus
11	604	32.7	609	1	KMLC_RAT	P20689 rattus norv
12	545.5	29.6	295	1	KMLC_DICDI	P25323 dictyosteli
13	532	28.8	474	1	KCC4_RAT	P13234 rattus norv
14	530.5	28.7	370	1	KCC1_HUMAN	Q14012 homo sapien
15	530.5	28.7	374	1	KCC1_RAT	Q63450 rattus norv
16	530	28.7	473	1	KCC4_HUMAN	Q16566 homo sapien
17	528.5	28.6	499	1	KCCD_HUMAN	Q13557 homo sapien
18	527.5	28.6	469	1	KCC4_MOUSE	P08414 mus musculu
19	526.5	28.5	533	1	KCCD_RAT	P15791 rattus norv
20	512	27.7	3038	1	TRIO_HUMAN	O75962 homo sapien
21	502	27.2	527	1	KCCG_RAT	P11730 rattus norv
22	493	26.7	424	1	KPSH_HUMAN	P11801 homo sapien
23	490.5	26.6	533	1	CDP2_ORYSA	P53683 oryza sativ
24	489.5	26.5	610	1	CDP1_ARATH	Q06850 arabidopsis
25	487.5	26.4	542	1	CDP3_ORYSA	P53684 oryza sativ
26	486.5	26.4	740	1	DCK1_HUMAN	O15075 homo sapien
27	486	26.3	478	1	KCCA_RAT	P11275 rattus norv
28	486	26.3	756	1	DCK1_MOUSE	Q9jlm8 mus musculu
29	485.5	26.3	433	1	DCK1_RAT	O08875 rattus norv
30	482.5	26.1	534	1	CDP1_ORYSA	P53682 oryza sativ
31	482	26.1	478	1	KCCA_MOUSE	P11798 mus musculu
32	481	26.1	542	1	KCCB_MOUSE	P28652 mus musculu
33	478.5	25.9	532	1	CDPK_DAUCA	P28582 daucus caro
34	478	25.9	542	1	KCCB_RAT	P08413 rattus norv
35	478	25.9	664	1	KCCB_HUMAN	Q13554 homo sapien
36	477.5	25.9	508	1	CDPK_SOYBN	P28583 glycine max
37	476.5	25.8	924	1	CSKP_MOUSE	O70589 mus musculu
38	476	25.8	513	1	CDP2_MAIZE	P49101 zea mays (m
39	475.5	25.8	909	1	CSKP_RAT	Q62915 rattus norv
40	475.5	25.8	921	1	CSKP_HUMAN	O14936 homo sapien
41	473.5	25.7	406	1	KPBH_RAT	P31325 rattus norv
42	472.5	25.6	406	1	KPBH_HUMAN	P15735 homo sapien
43	471	25.5	335	1	KCC1_SCHPO	Q9p7i2 schizosacch
44	469.5	25.4	406	1	KPBH_MOUSE	Q9db30 mus musculu
45	465.5	25.2	512	1	KI10_ARATH	Q38997 arabidopsis

ALIGNMENTS

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RESULT  1
DAPK_HUMAN
ID   DAPK_HUMAN      STANDARD;      PRT;  1431 AA.
AC   P53355;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).
GN   DAPK1 OR DAPK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95129831; PubMed=7828849;
RA   Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT   "Identification of a novel serine/threonine kinase and a novel 15-kD
RT   protein as potential mediators of the gamma interferon-induced cell
RT   death.";
RL   Genes Dev. 9:15-30(1995).
RN   [2]
RP   REVISIONS TO 164-171.
RA   Feinstein E.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC       DEATH.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X76104; CAA53712.1; -.
DR   HSSP; Q63450; 1A06.
DR   MIM; 600831; -.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00023; ank; 8.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00248; ANK; 7.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 6.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT   DOMAIN       13    266       PROTEIN KINASE.
FT   DOMAIN      267    334       CALMODULIN-BINDING.
FT   REPEAT      378    407       ANK 1.
FT   REPEAT      411    440       ANK 2.
FT   REPEAT      444    473       ANK 3.
FT   REPEAT      478    507       ANK 4.
FT   REPEAT      511    540       ANK 5.
FT   REPEAT      544    573       ANK 6.
FT   REPEAT      577    606       ANK 7.
FT   REPEAT      610    639       ANK 8.
FT   REPEAT      876    905       ANK 9.
FT   REPEAT     1163   1197       ANK 10.
FT   DOMAIN     1313   1397       DEATH.
FT   NP_BIND      19     27       ATP (BY SIMILARITY).
FT   BINDING      42     42       ATP (BY SIMILARITY).
FT   ACT_SITE    139    139       BY SIMILARITY.
FT   MUTAGEN      42     42       K->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   1431 AA;  160017 MW;  9EE84811004A155B CRC64;

  Query Match             70.0%;  Score 1293;  DB 1;  Length 1431;
  Best Local Similarity   68.2%;  Pred. No. 4.3e-71;
  Matches  242;  Conservative   62;  Mismatches   43;  Indels    8;  Gaps    2;

Qy       1 MEPFKQQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREE 60
           |  |:|: |:|:|| ||||||||||:||||||||||:|||||||||::::|||||||:
Db       1 MTVFRQENVDDYYDTGEELGSGQFAVVKKCREKSTGLQYAAKFIKKRRTKSSRRGVSRED 60

Qy      61 IEREVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFI 120
           ||||||||::: | ||||||:||||:|||: |||||:||||||||:||||:||||| |:
Db      61 IEREVSILKEIQHPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTEEEATEFL 120

Qy     121 KQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT 180
           ||||:|| |||: :|||||||||||||||:|:| | ||:|||||||:|: | ||||||||
Db     121 KQILNGVYYLHSLQIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFGNEFKNIFGT 180

Qy     181 PEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEF 240
           ||||||||||||||||||||||||||||||||||||||||||||||:::|:|:|::|:
Db     181 PEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANVSAVNYEFEDEY 240

Qy     241 FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQY 300
           ||:|| ||||||:|||| :|||:|||::|:|||| | | ||||: |: | ||::| |:|
Db     241 FSNTSALAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTQQALSRKASAVNMEKFKKFA 300

Qy     301 VRRRWKLSFSIVSLCNHLTRSLMKKVHL---RPDEDLRNCESDTEEDIARRKALH 352
             |:|| |  ::|||  |:|| : : ::   | |: |     | |:    :  :|
Db     301 ARKKWKQSVRLISLCQRLSRSFLSRSNMSVARSDDTL-----DEEDSFVMKAIIH 350


RESULT   2
KMLS_BOVIN
ID   KMLS_BOVIN     STANDARD;      PRT;  1176 AA.
AC   Q28824;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin].
GN   MYLK.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RX   MEDLINE=93203148; PubMed=1284247;
RA   Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
RA   Ebashi S.;
RT   "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
RT   myosin light chain kinase activity.";
RL   J. Biochem. 112:786-791(1992).
CC   -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
CC       SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC       IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
CC       FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SUBUNIT: TELOKIN BINDS CALMODULIN.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED BY
CC       ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
CC       FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
CC       NO CATALYTIC ACTIVITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S57131; AAB25794.1; -.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation.
FT   CHAIN         1   1176       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                ISOZYME.
FT   CHAIN      1022   1176       TELOKIN.
FT   INIT_MET   1022   1022       FOR TELOKIN.
FT   DOMAIN      100    291       16 X 12 AA TANDEM REPEATS.
FT   REPEAT      100    111       1.
FT   REPEAT      112    123       2.
FT   REPEAT      124    135       3 (INCOMPLETE).
FT   REPEAT      136    147       4.
FT   REPEAT      148    159       5.
FT   REPEAT      160    171       6.
FT   REPEAT      172    183       7.
FT   REPEAT      184    195       8.
FT   REPEAT      196    207       9.
FT   REPEAT      208    219       10.
FT   REPEAT      220    231       11.
FT   REPEAT      232    243       12.
FT   REPEAT      244    255       13.
FT   REPEAT      256    267       14.
FT   REPEAT      268    279       15.
FT   REPEAT      280    291       16.
FT   DOMAIN      603    673       FIBRONECTIN TYPE-III.
FT   DOMAIN      725    980       PROTEIN KINASE.
FT   DOMAIN      972   1035       CALMODULIN-BINDING.
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FT   DOMAIN     1084   1151       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND     731    739       ATP (BY SIMILARITY).
FT   BINDING     754    754       ATP (BY SIMILARITY).
FT   ACT_SITE    846    846       BY SIMILARITY.
FT   DOMAIN     1171   1176       POLY-GLU.
SQ   SEQUENCE   1176 AA;  128824 MW;  F53DC6D4D42D4B97 CRC64;


  Query Match           38.1%;  Score 703.5;  DB 1;  Length 1176;
  Best Local Similarity  42.5%;  Pred. No. 1.8e-35;
  Matches  149;  Conservative   62;  Mismatches  117;  Indels   23;  Gaps    7;

Qy       6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
           :||| ||||| | ||||:|  | :  || ||  :| || |   ::       :| | :|:
Db     718 EQKVSDFYDIEERLGSGKFGQVFRLVEKKTGKIWAGKFFKAYSAK------EKENIRQEI 771

Qy      66 SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
           ||:  : |  ::   | :| : ::| :||:|||||||: :  ::  |:| |   ::|||
Db     772 SIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMKQIS 831

Qy     125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
           :|| |:| : | | |||||||| ::|      ||||||||  :|:    | :|||||||
Db     832 EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV 889

Qy     185 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
           |||::||||:|   |||||||| |||:|| |||:||   |||||:|| ::|||:| |
Db     890 APEVINYEPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI 949

Qy     245 SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
           |: |||||  || |: : ||   : |:|||:     | :|       :: :  :|   ||
Db     950 SDDAKDFISNLLKKDMKNRLNCTQCLQHPWLMKDTKNMEA-----KKLSKDRMKKYMARR 1004

Qy     304 RWKLSFSIVSLCNHLTRSLM-------KKVHLRPDEDLRNCESDTEEDIAR 347
           :|: : : |     |:   |       |     |   | | |    ||:::
Db    1005 KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPL-NAEKLESEDVSQ 1054


RESULT   3
KMLS_HUMAN
ID   KMLS_HUMAN     STANDARD;      PRT;  1914 AA.
AC   Q15746; Q14844; Q16794; O95796; O95797; O95798; O95799; Q9UBG5;
AC   Q9UIT9;
DT   15-JUL-1998 (Rel. 36, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle and non-muscle isozymes
DE   (EC 2.7.1.117) (MLCK) [Contains: Telokin (Kinase related protein)
DE   (KRP)].
GN   MYLK OR MLCK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97304466; PubMed=9160829;
RA   Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.I., Gallagher P.J.,
RA   Verin A.D.;
RT   "Myosin light chain kinase in endothelium: molecular cloning and
RT   regulation.";
RL   Am. J. Respir. Cell Mol. Biol. 16:489-494(1997).
RN   [2]
RP   REVISIONS.
RA   Birukov K.G., Garcia J.G.N.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2; 3A; 3B AND 4).
RC   TISSUE=Umbilical vein;
RX   MEDLINE=99216419; PubMed=10198165;
RA   Lazar V.L., Garcia J.G.N.;
RT   "A single human myosin light chain kinase gene (MLCK; MYLK).";
RL   Genomics 57:256-267(1999).
RN   [4]
RP   REVISIONS TO ISOFORM 2.
RA   Birukov K.G., Garcia J.G.N.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 923-1914 FROM N.A.
RC   TISSUE=Hippocampus;
RX   MEDLINE=96121365; PubMed=8575746;
RA   Potier M.-C., Chelot E., Pekarsky Y., Gardiner K., Rossier J.,
RA   Turnell W.G.;
RT   "The human myosin light chain kinase (MLCK) from hippocampus:
RT   cloning, sequencing, expression, and localization to 3qcen-q21.";
RL   Genomics 29:562-570(1995).
RN   [6]
RP   SEQUENCE OF 1614-1914 FROM N.A.
RC   TISSUE=Lung, and Placenta;
RX   MEDLINE=20007838; PubMed=10536370;
RA   Watterson D.M., Schavocky J.P., Guo L., Weiss C., Chlenski A.,
RA   Shrinsky V.P., Van Eldik L.J., Haiech J.;
RT   "Analysis of the kinase-related protein gene found at human chromosome
RT   3q21 in a multi-gene cluster: organization, expression, alternative
RT   splicing and polymorphic marker.";
RL   J. Cell. Biochem. 75:481-491(1999).
RN   [7]
RP   SEQUENCE OF 1456-1914 FROM N.A.
RC   TISSUE=Placenta;
RA   Watterson M.D.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
CC       SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC       IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
CC       FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL
CC       DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE
CC       EDEMA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO
CC       CONTROL THE GROWTH INITIATION OF ASTROCYTIC PROCESSES IN CULTURE
CC       AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED
CC       BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT
CC       IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SUBUNIT: TELOKIN BINDS CALMODULIN.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE
CC       LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL
CC       SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
CC       INITIATION.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3A,
CC       3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
CC       EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
CC       CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO BE
CC       NEITHER TISSUE- NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS
CC       THE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN
CC       HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
CC   -!- PTM: MLCK IS PROBABLY DOWN-REGULATED BY PHOSPHORYLATION.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U48959; AAC18423.2; -.
DR   EMBL; AF069601; AAD15921.2; -.
DR   EMBL; AF069602; AAD15922.1; -.
DR   EMBL; AF069603; AAD15923.1; -.
DR   EMBL; AF069604; AAD15924.1; -.
DR   EMBL; X85337; CAA59685.1; -.
DR   EMBL; AF096771; AAD51380.1; -.
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DR   EMBL; AF096766; AAD51380.1; JOINED.
DR   EMBL; AF096767; AAD51380.1; JOINED.
DR   EMBL; AF096768; AAD51380.1; JOINED.
DR   EMBL; AF096769; AAD51380.1; JOINED.
DR   EMBL; AF096770; AAD51380.1; JOINED.
DR   EMBL; AF096774; AAD54018.1; -.
DR   EMBL; AF096771; AAD51381.1; -.
DR   EMBL; AF096769; AAD51381.1; JOINED.
DR   EMBL; AF096770; AAD51381.1; JOINED.
DR   EMBL; X90870; CAA62378.1; -.
DR   HSSP; P56276; 1TLK.
DR   MIM; 600922; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 8.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 8.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation; Alternative splicing.
FT   CHAIN         1   1914       MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT                                ISOZYME.
FT   CHAIN       923   1914       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                ISOZYME.
FT   CHAIN      1761   1914       TELOKIN.
FT   INIT_MET    923    923       FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH-
FT                                MUSCLE ISOZYME.
FT   INIT_MET   1761   1761       FOR TELOKIN.
FT   DOMAIN     1343   1413       FIBRONECTIN TYPE-III.
FT   DOMAIN     1464   1719       PROTEIN KINASE.
FT   DOMAIN     1711   1774       CALMODULIN-BINDING.
FT   DOMAIN     1824   1891       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND    1470   1478       ATP (BY SIMILARITY).
FT   BINDING    1493   1493       ATP (BY SIMILARITY).
FT   ACT_SITE   1585   1585       BY SIMILARITY.
FT   DOMAIN     1906   1914       POLY-GLU.
FT   DOMAIN      868    998       5 X 28 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT      868    895       I-1.
FT   REPEAT      896    923       I-2.
FT   REPEAT      924    951       I-3.
FT   REPEAT      952    979       I-4.
FT   REPEAT      980    998       I-5 (INCOMPLETE).
FT   DOMAIN      999   1063       6 X 12 AA APPROXIMATE TANDEM REPEATS.
FT   REPEAT      999   1003       II-1 (INCOMPLETE).
FT   REPEAT     1004   1015       II-2.
FT   REPEAT     1016   1027       II-3.
FT   REPEAT     1028   1039       II-4.
FT   REPEAT     1040   1051       II-5.
FT   REPEAT     1052   1063       II-6.
FT   VARSPLIC    437    506       VSGIPKPEVAWFLEGTPVRRQEGSIEVYEDAGSHYLCLLKA
FT                                RTRDSGTYSCTASNAQGQVSCSWTLQVER -> G (IN
FT                                ISOFORM 2 AND ISOFORM 3B).
FT   VARSPLIC   1433   1439       DEVEVSD -> MKWRCQT (IN ISOFORM 3A,
FT                                ISOFORM 3B AND ISOFORM 4).
FT   VARSPLIC   1473   1546       GKFGQVFRLVEKKTRKVWAGKFFKAYSAKEKENIRQEISIM
FT                                NCLHHPKLVQCVDAFEEKANIVMVLEIVSGGEL -> L
FT                                (IN ISOFORM 4).
FT   VARSPLIC   1655   1705       MISSING (IN ISOFORM 3A AND ISOFORM 3B).
FT   VARSPLIC   1790   1790       MISSING (IN ISOFORM DEL-1790).
FT   CONFLICT    933    933       V -> M (IN REF. 5).
FT   CONFLICT    963    963       S -> P (IN REF. 3; AAD15922).
FT   CONFLICT   1022   1022       P -> A (IN REF. 5).
FT   CONFLICT   1048   1050       KPM -> EAH (IN REF. 5).
FT   CONFLICT   1162   1162       P -> L (IN REF. 3; AAD15922 AND
FT                                AAD15923).
FT   CONFLICT   1210   1210       L -> P (IN REF. 5).
FT   CONFLICT   1280   1280       E -> D (IN REF. 3; AAD15922 AND
FT                                AAD15923).
FT   CONFLICT   1284   1284       M -> I (IN REF. 3; AAD15922, AAD15923 AND
FT                                AAD15924).
FT   CONFLICT   1300   1300       A -> G (IN REF. 5).
FT   CONFLICT   1316   1316       L -> S (IN REF. 5).
FT   CONFLICT   1326   1326       T -> S (IN REF. 5).
FT   CONFLICT   1478   1478       V -> C (IN REF. 5).
FT   CONFLICT   1511   1511       S -> T (IN REF. 3; AAD15922 AND
FT                                AAD15923).
FT   CONFLICT   1563   1563       I -> T (IN REF. 5).
FT   CONFLICT   1609   1609       A -> P (IN REF. 5).
FT   CONFLICT   1639   1639       G -> R (IN REF. 5).
FT   CONFLICT   1639   1640       GY -> D (IN REF. 3; AAD15922, AAD15923

  Query Match           37.8%;  Score 698;  DB 1;  Length 1914;
  Best Local Similarity  41.6%;  Pred. No. 6.7e-35;
  Matches  146;  Conservative   66;  Mismatches  117;  Indels   22;  Gaps    6;

Qy       6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
           :||| ||||| | ||||:|  | :  || |   :| || |   ::       :| | :|:
Db    1457 EQKVSDFYDIEERLGSGKFGQVFRLVEKKTRKVWAGKFFKAYSAK------EKENIRQEI 1510

Qy      66 SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
           ||:  : |  ::   | :| : ::| :||:||||||: :  ::  |:| |   :::||
Db    1511 SIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQIS 1570

Qy     125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
           :|| |:| : | | |||||||| ::|      |||||||||  :|:    | :|||||||
Db    1571 EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV 1628

Qy     185 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
           |||::||||:|   |||||||| |||:|| |||:||   |||||:|| ::|||:| |
Db    1629 APEVINYEPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI 1688

Qy     245 SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
           |: ||||| || |: : ||   : |:|||:     | :|       :: :  :|   ||
Db    1689 SDDAKDFISNLLKKDMKNRLDCTQCLQHPWLMKDTKNMEA-----KKLSKDRMKKYMARR 1743

Qy     304 RWKLSFSIVSLCNHLTRSLM-------KKVHLRPDEDLRNCESDTEEDIAR 347
           :|: : : |     |:   |        |      |   |   : ::|||:::
Db    1744 KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLNAEKLESEEDVSQ 1794


RESULT   4
KMLS_RABIT
ID   KMLS_RABIT     STANDARD;      PRT;  1147 AA.
AC   P29294; Q28729;
DT   01-DEC-1992 (Rel. 24, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin].
GN   MYLK.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Smooth muscle;
RX   MEDLINE=92084694; PubMed=1748666;
RA   Gallagher P.J., Herring B.P., Griffin S.A., Stull J.T.;
RT   "Molecular characterization of a mammalian smooth muscle myosin light
RT   chain kinase.";
RL   J. Biol. Chem. 266:23936-23944(1991).
RN   [2]
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RP   SEQUENCE OF 993-1147 FROM N.A. (TELOKIN).
RX   MEDLINE=92084695; PubMed=1748667;
RA   Gallagher P.J., Herring B.P.;
RT   "The carboxyl terminus of the smooth muscle myosin light chain kinase
RT   is expressed as an independent protein, telokin.";
RL   J. Biol. Chem. 266:23945-23952(1991).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED
CC       BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
CC       FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
CC       NO CATALYTIC ACTIVITY).
CC   -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M76233; AAA73093.1; -.
DR   EMBL; M76234; AAA31408.1; -.
DR   EMBL; M76181; AAA31409.1; -.
DR   PIR; A41675; A41675.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation.
FT   CHAIN         1   1147       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                ISOZYME.
FT   CHAIN       993   1147       TELOKIN.
FT   INIT_MET    993    993       FOR TELOKIN.
FT   DOMAIN      100    288       16 X 12 AA TANDEM REPEATS.
FT   REPEAT      100    111       1.
FT   REPEAT      112    123       2.
FT   REPEAT      124    132       3 (INCOMPLETE).
FT   REPEAT      133    144       4.
FT   REPEAT      145    156       5.
FT   REPEAT      157    168       6.
FT   REPEAT      169    180       7.
FT   REPEAT      181    192       8.
FT   REPEAT      193    204       9.
FT   REPEAT      205    216       10.
FT   REPEAT      217    228       11.
FT   REPEAT      229    240       12.
FT   REPEAT      241    252       13.
FT   REPEAT      253    264       14.
FT   REPEAT      265    276       15.
FT   REPEAT      277    288       16.
FT   DOMAIN      574    644       FIBRONECTIN TYPE-III.
FT   DOMAIN      696    951       PROTEIN KINASE.
FT   DOMAIN      943   1006       CALMODULIN-BINDING.
FT   DOMAIN     1056   1123       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND     702    710       ATP (BY SIMILARITY).
FT   BINDING     725    725       ATP (BY SIMILARITY).
FT   ACT_SITE    817    817       BY SIMILARITY.
FT   DOMAIN     1138   1147       POLY-GLU.
FT   CONFLICT   1114   1114       C -> R (IN REF. 2).
SQ   SEQUENCE   1147 AA;  125719 MW;  F039E624C6E31024 CRC64;


  Query Match             37.6%;  Score 694;  DB 1;  Length 1147;
  Best Local Similarity   41.6%;  Pred. No. 6.5e-35;
  Matches  146;  Conservative   63;  Mismatches  120;  Indels   22;  Gaps    6;

Qy       6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
           :||| ||||| | ||||:|  | :  || ||  :| || |   ::       :| |  |:
Db     689 EQKVSDFYDIEERLGSGKFGQVFRLVEKKTGKIWAGKFFKAYSAK------EKENIPAEI 742

Qy      66 SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
             |:  : |  ::   | :| : ::| :||:|||||||: :  ::  |:| |   :::||
Db     743 GIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQIS 802

Qy     125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
           :|| |:| : | | |||||||| ::|      |||||||||  :|:    | :|||||||
Db     803 EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV 860

Qy     185 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
           |||::||||:    |||||||| |||:|| |||:||   |||||:|| ::|||:| |
Db     861 APEVINYEPISYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI 920

Qy     245 SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
           |: |||||  || |: : ||  : |:|||:     | :|       :: :  :|   ||
Db     921 SDDAKDFISNLLKKDMKNRLDCTQCLQHPWLMKDTKNMEA-----KKLSKDRMKKYMARR 975

Qy     304 RWKLSFSIVSLCNHLTRSLM-------KKVHLRPDEDLRNCESDTEEDIAR 347
           :|: : : |     |:   |       |     |   |     :||||:::
Db     976 KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLTAERLETEEDVSQ 1026


RESULT   5
KMLS_CHICK
ID   KMLS_CHICK     STANDARD;      PRT;  1906 AA.
AC   P11799; P19038;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle and non-muscle isozymes
DE   (EC 2.7.1.117) (MLCK) [Contains: Telokin].
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (MLCK-210).
RX   MEDLINE=96033976; PubMed=7589469;
RA   Watterson D.M., Collinge M., Lukas T.J., van Eldik L.J., Birukov K.G.,
RA   Stepanova O.V., Shirinsky V.P.;
RT   "Multiple gene products are produced from a novel protein kinase
RT   transcription region.";
RL   FEBS Lett. 373:217-220(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (MLCK-108).
RX   MEDLINE=90192792; PubMed=2315320;
RA   Olson N.J., Pearson R.B., Needleman D.S., Hurwitz M.J., Kemp B.E.,
RA   Means A.R.;
RT   "Regulatory and structural motifs of chicken gizzard myosin light
RT   chain kinase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).
RN   [3]
RP   SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Fibroblast;
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RX   MEDLINE=90361738; PubMed=2202734;
RA   Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski A.P.,
RA   Matrisian P.E., Guerra-Santos L., Wilson E., Lukas T.J.,
RA   van Eldik L.J., Watterson D.M.;
RT   "Use of DNA sequence and mutant analyses and antisense
RT   oligodeoxynucleotides to examine the molecular basis of nonmuscle
RT   myosin light chain kinase autoinhibition, calmodulin recognition, and
RT   activity.";
RL   J. Cell Biol. 111:1107-1125(1990).
RN   [4]
RP   SEQUENCE OF 1259-1906 FROM N.A.
RC   TISSUE=Gizzard;
RX   MEDLINE=87157587; PubMed=3030394;
RA   Guerriero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.;
RT   "Domain organization of chicken gizzard myosin light chain kinase
RT   deduced from a cloned cDNA.";
RL   Biochemistry 25:8372-8381(1986).
RN   [5]
RP   SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RC   TISSUE=Gizzard;
RX   MEDLINE=93073972; PubMed=1444462;
RA   Yoshikai S., Ikebe M.;
RT   "Molecular cloning of the chicken gizzard telokin gene and cDNA.";
RL   Arch. Biochem. Biophys. 299:242-247(1992).
RN   [6]
RP   SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RX   MEDLINE=92236611; PubMed=1373815;
RA   Collinge M., Matrisian P.E., Zimmer W.E., Shattuck R.L., Lukas T.J.,
RA   van Eldik L.J., Watterson D.M.;
RT   "Structure and expression of a calcium-binding protein gene contained
RT   within a calmodulin-regulated protein kinase gene.";
RL   Mol. Cell. Biol. 12:2359-2371(1992).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/
CC       MLCK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE
CC       TRANSDUCTION OF CALCIUM SIGNALS.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED
CC       BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (MLCK-210; WHICH IS
CC       THE LONGEST FORM); A SMOOTH-MUSCLE FORM (MLCK-108) AND TELOKIN (A
CC       C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
CC   -!- TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG,
CC       INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE
CC       EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE GIZZARD.
CC   -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X52876; CAA37056.1; -.
DR   EMBL; X52876; CAA37057.1; -.
DR   EMBL; X52876; CAA37058.1; -.
DR   EMBL; M31048; AAA49069.1; -.
DR   EMBL; M14953; AAA69964.1; -.
DR   EMBL; M96655; AAA49083.1; -.
DR   EMBL; M88283; AAA48647.1; -.
DR   EMBL; M88284; AAB53768.1; -.
DR   PIR; A25810; A25810.
DR   PIR; A37099; A37099.
DR   PIR; S11652; S11652.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 9.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 8.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW   Alternative initiation.
FT   CHAIN         1   1906       MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT                                ISOZYME (MLCK-210).
FT   CHAIN       935   1906       MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT                                ISOZYME (MLCK-108).
FT   CHAIN      1750   1906       TELOKIN.
FT   INIT_MET    935    935       FOR MLCK-108.
FT   INIT_MET   1750   1750       FOR TELOKIN.
FT   DOMAIN     1330   1400       FIBRONECTIN TYPE-III.
FT   DOMAIN     1453   1708       PROTEIN KINASE.
FT   DOMAIN     1809   1876       IG-LIKE C2-TYPE DOMAIN.
FT   NP_BIND    1459   1467       ATP (BY SIMILARITY).
FT   BINDING    1482   1482       ATP (BY SIMILARITY).
FT   ACT_SITE   1574   1574       BY SIMILARITY.
FT   DOMAIN     1716   1728       CALMODULIN AUTOINHIBITION (AM13) REGION
FT                                (POTENTIAL).
FT   DOMAIN     1730   1749       CALMODULIN RECOGNITION (RS20) REGION
FT                                (POTENTIAL).
FT   DOMAIN     1317   1364       MOTIF IA.
FT   DOMAIN     1385   1402       MOTIF IB.
FT   DOMAIN      660   1833       4 X REPEATS, MOTIF IIA.
FT   REPEAT      660    676       IIA-1.
FT   REPEAT      758    774       IIA-2.
FT   REPEAT     1107   1123       IIA-3.
FT   REPEAT     1817   1833       IIA-4.
FT   DOMAIN      693   1866       5 X REPEATS, MOTIF IIB.
FT   REPEAT      693    708       IIB-1.
FT   REPEAT      791    807       IIB-2.
FT   REPEAT     1140   1156       IIB-3.
FT   REPEAT     1281   1297       IIB-4.
FT   REPEAT     1851   1866       IIB-5.
FT   DOMAIN      970   1226       4 X REPEATS, MOTIF III.
FT   REPEAT      970    987       III-1.
FT   REPEAT      999   1016       III-2.
FT   REPEAT     1061   1078       III-3.
FT   REPEAT     1209   1226       III-4.
FT   DOMAIN     1700   1763       CALMODULIN-BINDING.
FT   DOMAIN     1896   1906       POLY-GLU.
FT   MOD_RES    1748   1748       PHOSPHORYLATION.
FT   MOD_RES    1762   1762       PHOSPHORYLATION.
FT   CONFLICT   1439   1439       R -> Q (IN REF. 4).
SQ   SEQUENCE   1906 AA;  210445 MW;  AD7D8A3B69EE3363 CRC64;

  Query Match             37.1%;  Score 685.5;  DB 1;  Length 1906;
  Best Local Similarity   43.8%;  Pred. No. 3.8e-34;
  Matches  140;  Conservative   58;  Mismatches  107;  Indels   15;  Gaps    5;

Qy       6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
           :||| | |:| | ||||:|  | :  || ||  :| || |   ::       :| |  |:
Db    1446 EQKVSDVYNIEERLGSGKFGQVFRLVEKKTGKVWAGKFFKAYSAK------EKENIRDEI 1499

Qy      66 SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
           ||:  : |  ::   | :| : ::| :||:|||||||: :  ::  |:| |   :::||
Db    1500 SIMNCLHHPKLVQCVDAFEEKANIVMVLEMVSGGELFERIIDEDFELTERECIKYMRQIS 1559

Qy     125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
           :|| |:| : | | |||||||| ::|      |||||||||  :|     | :|||||||
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Db   1560 EGVEYIHKQGIVHLDLKPENIMCVNKT--GTSIKLIDFGLARRLESAGSLKVLFGTPEFV 1617

Qy    185 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
          |||::||||:| | |||||||| |||:|| ||||:||   |||||:|| ::|||:| |
Db   1618 APEVINYEPIGYETDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI 1677

Qy    245 SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
          |: |||||  || |: : ||   : |:|||:     | :|       :: :  :|   ||
Db   1678 SDDAKDFISNLLKKDMKSRLNCTQCLQHPWLQKDTKNMEA-----KKLSKDRMKKYMARR 1732

Qy    304 RWKLSFSIVSLCNHLTRSLM 323
          :|: :   |     |:   |
Db   1733 KWQKTGHAVRAIGRLSSMAM 1752


RESULT   6
S17A_HUMAN
ID   S17A_HUMAN     STANDARD;      PRT;   414 AA.
AC   Q9UEE5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 1).
GN   STK17A OR DRAK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-90.
RC   TISSUE=Placenta, and Liver;
RX   MEDLINE=99003259; PubMed=9786912;
RA   Sanjo H., Kawai T., Akira S.;
RT   "DRAKs, novel serine/threonine kinases related to death-associated
RT   protein kinase that trigger apoptosis.";
RL   J. Biol. Chem. 273:29066-29071(1998).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
CC       EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
CC       TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
CC       INITIATION OF APOTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN LOWER
CC       LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AB011420; BAA34126.1; -.
DR   HSSP; P00518; 1PHK.
DR   MIM; 604726; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       61     321       PROTEIN KINASE.
FT   DOMAIN       33      37       POLY-PRO.
FT   NP_BIND      67      75       ATP (BY SIMILARITY).
FT   BINDING      90      90       ATP (BY SIMILARITY).
FT   MUTAGEN      90      90       K->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   414 AA;  46559 MW;  0C140290438C2A1A CRC64;

  Query Match           36.2%;  Score 668.5;  DB 1;  Length 414;
  Best Local Similarity  38.9%;  Pred. No. 7e-34;
  Matches  139;  Conservative   78;  Mismatches   95;  Indels   45;  Gaps    9;

Qy      2 EPFKQQKVEDFYDI--GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-R 58
          |||     :| | :  | ||| |:||:|:|| :| :| |:||||::||     |:|   |
Db     53 EPF-----QDGYSLCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKR-----RKGQDCR 102

Qy     59 EEIEREVSILRQVLHHN--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEE 114
           ||  |:::| ::   |  || ||:|||  :::: :||  :|||:||     ::|:  |:
Db    103 MEIIHEIAVL-ELAQDNPWVINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEK 161

Qy    115 EATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEF 174
          :    ::|||:|||::|||: : | ||||:||:|  :: |:  ||::||||:  :::  |
Db    162 DVQRLMRQILEGVHFLHTRDVVHLDLKPQNILLTSES-PLGDIKIVDFGLSRILKNSEEL 220

Qy    175 KNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSY 234
          : | ||||:|||||::|:|: :  |||||||:||::|:| |||||: |||  ||: ::
Db    221 REIMGTPEYVAPEILSYDPISMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNL 280

Qy    235 DFDEEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLE 294
          : || |   || | |||| ||||:   | | :| |:|||:|    |:   | |  :
Db    281 SYSEEEFDVLSESAVDFIRTLLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEA 340

Qy    295 NFRKQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKAL 351
          |                            ::: |  |: :    :|:||| |   : :
Db    341 N-------------------------ALQEGHSVPEINSDTDKSETEESIVTEELI 371


RESULT   7
S17A_RABIT
ID   S17A_RABIT     STANDARD;      PRT;   397 AA.
AC   Q9GM70;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 1) (rDRAK1).
GN   STK17A OR DRAK1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Osteoclast;
RX   MEDLINE=21276420; PubMed=11279167;
RA   Kojima H., Nemoto A., Uemura T., Honma R., Ogura M., Liu Y.-K.;
RT   "rDRAK1, a novel kinase related to apoptosis, is strongly expressed in
RT   active osteoclasts and induces apoptosis.";
RL   J. Biol. Chem. 276:19238-19243(2001).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) (BY
CC       SIMILARITY) AND IS INVOLVED IN OSTEOCLAST APOPTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BONE MARROW AND IN LOWER
CC       LEVELS IN BRAIN, HEART, LUNG, LIVER AND KIDNEY.
CC   -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB042195; BAB16111.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
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DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       44     304       PROTEIN KINASE.
FT   NP_BIND      50     58        ATP (BY SIMILARITY).
FT   BINDING      73     73        ATP (BY SIMILARITY).
SQ   SEQUENCE   397 AA;  44462 MW;  589041E107F50097 CRC64;

  Query Match           35.7%;  Score 659.5;  DB 1;  Length 397;
  Best Local Similarity 43.5%;  Pred. No. 2.3e-33;
  Matches  131;  Conservative   70;  Mismatches   81;  Indels   19;  Gaps    8;

Qy       2 EPFKQQKVEDFYDI--GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-R 58
           |||     :| | :  | ||| |:||:|:|| :| :| |:||||::||     |:|   |
Db      36 EPF-----QDCYSLSPGRELGRGKFAVVRKCIQKDSGKEFAAKFMRKR-----RKGQDCR 85

Qy      59 EEIEREVSILRQVLHHN--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEE 114
             ||  |:::| ::   |  || ||:|||  :::: :|| :|||: |     : |: :|:
Db      86 MEIIHEIAVL-ELAQDNPWVINLHEVYETSSEMILVLEYAAGGEISDQCVADRDEAFNEK 144

Qy     115 EATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEF 174
           :    ::|||:||::|||  : | ||||:||:|  :: |:  ||::|||||:  ::: |
Db     145 DVQRLMRQILEGVHFLHTHDVVHLDLKPQNILLTSES-PLGDIKIVDFGLSRIVKNSEEL 203

Qy     175 KNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSY 234
           : | ||||:|||||::|:|: :  |||||||:||::|:| |||||| |||| ||: ::
Db     204 REIMGTPEYVAPEILSYDPISMATDMWSIGVLTYVMLTGISPFLGDNKQETFLNISQMNL 263

Qy     235 DFDEEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLE 294
           : || |   || | |||:|||||:   | | :| |:|||:|    |  ::| : :
Db     264 SYSEEEFDTVSESAVDFIKKLLVKKPEDRATAEECLKHPWLTQSSIQDPVLRVKEALEEA 323

Qy     295 N 295
           |
Db     324 N 324


RESULT   8
S17B_HUMAN
ID   S17B_HUMAN     STANDARD;      PRT;   372 AA.
AC   O94768;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine kinase 17B (EC 2.7.1.-) (DAP kinase-related
DE   apoptosis-inducing protein kinase 2).
GN   STK17B OR DRAK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-62.
RC   TISSUE=Placenta, and Liver;
RX   MEDLINE=99003259; PubMed=9786912;
RA   Sanjo H., Kawai T., Akira S.;
RT   "DRAKs, novel serine/threonine kinases related to death-associated
RT   protein kinase that trigger apoptosis.";
RL   J. Biol. Chem. 273:29066-29071(1998).
CC   -!- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
CC       EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
CC       TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
CC       INITIATION OF APOTOSIS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, LUNG, PANCREAS
CC       AND IN LOWER LEVELS IN HEART, BRAIN, LIVER, SKELETAL MUSCLE AND
CC       KIDNEY.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB011421; BAA34127.1; -.
DR   HSSP; P00518; 1PHK.
DR   MIM; 604727; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Nuclear protein; Apoptosis.
FT   DOMAIN       33     293       PROTEIN KINASE.
FT   DOMAIN      308     311       POLY-SER.
FT   NP_BIND      39      47       ATP (BY SIMILARITY).
FT   BINDING      62      62       ATP (BY SIMILARITY).
FT   MUTAGEN      62      62       K->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   372 AA;  42344 MW;  7E69FFAED6DC1FF3 CRC64;

  Query Match           34.8%;  Score 641.5;  DB 1;  Length 372;
  Best Local Similarity 46.8%;  Pred. No. 2.7e-32;
  Matches  132;  Conservative   49;  Mismatches   90;  Indels   11;  Gaps    6;

Qy       3 PFKQQKVEDFYDI-GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REE 60
           | | :   :|| :  :||| |:||:|::|  |||| ||||||:|||     |||   | |
Db      22 PIKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYAAKFLKKR-----RRGQDCRAE 76

Qy      61 IEREVSILRQVLH-HNVITLHDVYENRTDVVHILELVSGGELFDFLAQK--ESLSEEEAT 117
           |  |:::|         || ||:|||| :::: |||  :|||:|     :  | :|| :
Db      77 ILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFSLCLPELAEMVSENDVI 136

Qy     118 SFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNI 177
           |||||:|| |||   | | ||||:|| ||    |:  ||::|||:: :|    | : |
Db     137 RLIKQILEGVYYLHQNNIVHLDLKPQNI-LLSSIYPLGDIKIVDFGMSRKIGHACELREI 195

Qy     178 FGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFD 237
           ||||::||||:||:|:    |||:||:| |:||:  |||:|:  |||  ||: |: |:
Db     196 MGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDNQETYLNISQVNVDYS 255

Qy     238 EEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVD 279
           || ||  |:|| |||: ||||   || | :  | | |:   |
Db     256 EETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSWLQQWD 297


RESULT   9
KMLS_SHEEP
ID   KMLS_SHEEP     STANDARD;      PRT;   438 AA.
AC   O02827;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE   [Contains: Telokin] (Fragment).
GN   MYLK.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139839; PubMed=8569750;
RA   Pato M.D., Kerc E., Lye S.J.;
RT   "Phosphorylation and partial sequence of pregnant sheep myometrium
RT   myosin light chain kinase.";
RL   Mol. Cell. Biochem. 149:59-65(1995).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- DOMAIN: TELOKIN BINDS CALMODULIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S80867; AAB50715.2; -.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Immunoglobulin domain.
FT   NON_TER       1      1
FT   DOMAIN       <1    241       PROTEIN KINASE.
FT   DOMAIN      233    296       CALMODULIN-BINDING.
FT   DOMAIN      346    413       IG-LIKE C2-TYPE DOMAIN.
FT   BINDING      15     15       ATP (BY SIMILARITY).
FT   ACT_SITE    107    107       BY SIMILARITY.
FT   DOMAIN      283    438       TELOKIN.
FT   DOMAIN      433    438       POLY-GLU.
SQ   SEQUENCE   438 AA;  49503 MW;  77A02F4885A10B51 CRC64;


  Query Match             34.5%;  Score 637;  DB 1;  Length 438;
  Best Local Similarity   40.9%;  Pred. No. 6.1e-32;
  Matches  133;  Conservative   61;  Mismatches  109;  Indels   22;  Gaps    6;

Qy      32 EKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNVITLHDVYENRTDVVH 91
           || ||  :| || |   ::       :| | :|:||:  : |  ::   | :| : ::|
Db       5 EKKTGKVWAGKFFKAYSAK------EKENIRQEISIMNCLHHPKLVQCVDAFEEKANIVM 58

Qy      92 ILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDK 150
           :||:|||||||: :  ::  |:| |   ::||| :|| |:| : | | |||||||| ::|
Db      59 VLEIVSGGELFERIIDEDFELTERECIKYMKQISEGVEYIHKQGIVHLDLKPENIMCVNK 118

Qy     151 NIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL 210
           |||||||||  :|:    | :||||||||||::||||:|   |||||||| |||
Db     119 T--GTRIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINYEPIGYATDMWSIGVICYIL 176

Qy     211 LSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKLLVKETRKRLTIQEAL 270
           :|| |||:||   |||||:|| ::|||:| |   |: ||||| || |: : ||   : |
Db     177 VSGLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDFISNLLKKDIKNRLNCTQCL 236

Qy     271 RHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRRRWKLSFSIVSLCNHLTRSLM------ 323
           :|||:     | :|       ::    :|   ||:|: : : |     |:   |
Db     237 QHPWLXXXTKNMEA-----KKLSKHRMKKYMARRKWQKTGNAVRAIGRLSSMAMISGLSG 291

Qy     324 -KKVHLRPDEDLRNCESDTEEDIAR 347
            |    |   |   : ::|||:::
Db     292 RKSSTGSPTSPLNAEKLESEEDVSQ 316


RESULT  10
KMLC_RABIT
ID   KMLC_RABIT     STANDARD;      PRT;   607 AA.
AC   P07313;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90110242; PubMed=1688558;
RA   Herring B.P., Stull J.T., Gallagher P.J.;
RT   "Domain characterization of rabbit skeletal muscle myosin light chain
RT   kinase.";
RL   J. Biol. Chem. 265:1724-1730(1990).
RN   [2]
RP   SEQUENCE OF 1-603.
RX   MEDLINE=87101105; PubMed=3542042;
RA   Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
RT   "Amino acid sequence of rabbit skeletal muscle myosin light chain
RT   kinase.";
RL   Biochemistry 25:8049-8057(1986).
RN   [3]
RP   SEQUENCE OF 295-603.
RX   MEDLINE=86104095; PubMed=3841288;
RA   Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
RA   Titani K.;
RT   "Amino acid sequence of an active fragment of rabbit skeletal muscle
RT   myosin light chain kinase.";
RL   Biochemistry 24:6028-6037(1985).
RN   [4]
RP   STRUCTURE BY NMR OF 577-602.
RX   MEDLINE=92263094; PubMed=1585175;
RA   Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
RT   "Solution structure of a calmodulin-target peptide complex by
RT   multidimensional NMR.";
RL   Science 256:632-638(1992).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J05194; AAA31400.1; -.
DR   PIR; A25830; A25830.
DR   PIR; A05120; A05120.
DR   PIR; A35021; A35021.
DR   PDB; 2BBM; 31-JAN-94.
DR   PDB; 2BBN; 31-JAN-94.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
```

```
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Acetylation; 3D-structure.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION.
FT   DOMAIN      296    551       PROTEIN KINASE.
FT   DOMAIN      585    597       CALMODULIN-BINDING.
FT   NP_BIND     302    310       ATP (BY SIMILARITY).
FT   BINDING     325    325       ATP (BY SIMILARITY).
FT   ACT_SITE    417    417       BY SIMILARITY.
FT   CONFLICT    335    335       K -> KK (IN REF. 2 AND 3).
FT   HELIX       581    595
FT   TURN        596    596
SQ   SEQUENCE   607 AA;  65337 MW;  6E677641751A04C8 CRC64;
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  Query Match             32.8%;  Score 605;  DB 1;  Length 607;
  Best Local Similarity   40.4%;  Pred. No. 7.7e-30;
  Matches  124;  Conservative   63;  Mismatches  106;  Indels   14;  Gaps    5;

Qy      17 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNV 76
           | || |:|  |  | |||||: ||| |||:  :       :| :  |: :: |: | |:
Db     300 EALGGGKFGAVCTCTEKSTGLKLAAKVIKKQTPK------DKEMVMLEIEVMNQLNHRNL 353

Qy      77 ITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLHTKKI 135
           | |:   |   ::|  :| : |||||: :  ::  |:| :   |::|| ||: ::|  ::
Db     354 IQLYAAIETPHEIVLFMEYIEGGELFERIVDEDYHLTEVDTMVFVRQICDGILFMHKMRV 413

Qy     136 AHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLG 195
            | |||||||: ::    :  :|:|||||||       : |  |||||::||:|||: :
Db     414 LHLDLKPENILCVNTTGHL--VKIIDFGLARRYNPNEKLKVNFGTPEFLSPEVVNYDQIS 471

Qy     196 LEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKL 255
            : ||||:|||||:|||| ||||||   ||| |: | :: |||| |   |: ||||:  |
Db     472 DKTDMWSLGVITYMLLSGLSPFLGDDDTETLNNVLSGNWYFDEETFEAVSDEAKDFVSNL 531

Qy     256 LVKETRKRLTIQEALRHPWITPVDNQQAMVRR--ESVVNLENFRKQYVRRRWKLSFSIVS 313
           :|||   |::  : | |||:  :  :     | :| : |   :|  ::|||| :|  ||
Db     532 IVKEQGARMSAAQCLAHPWLNNLAEKAKRCNRRLKSQILL---KKYLMKRRWKKNFIAVS 588

Qy     314 LCNHLTR 320
             |   :
Db     589 AANRFKK 595
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RESULT  11
KMLC_RAT
ID   KMLC_RAT       STANDARD;      PRT;   609 AA.
AC   P20689;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88273159; PubMed=2839493;
RA   Roush C.L., Kennelly P.J., Glaccum M.B., Helfman D.M., Scott J.D.,
RA   Krebs E.G.;
RT   "Isolation of the cDNA encoding rat skeletal muscle myosin light
RT   chain kinase. Sequence and tissue distribution.";
RL   J. Biol. Chem. 263:10510-10516(1988).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03886; AAA41625.1; ALT_SEQ.
DR   PIR; A28798; A28798.
DR   HSSP; P00518; 1PHK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   ATP-binding; Phosphorylation; Acetylation.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DOMAIN      298    553       PROTEIN KINASE.
FT   DOMAIN      587    599       CALMODULIN-BINDING (BY SIMILARITY).
FT   NP_BIND     304    312       ATP (BY SIMILARITY).
FT   BINDING     327    327       ATP (BY SIMILARITY).
FT   ACT_SITE    419    419       BY SIMILARITY.
SQ   SEQUENCE   609 AA;  65685 MW;  0073A22659BD1358 CRC64;
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  Query Match             32.7%;  Score 604;  DB 1;  Length 609;
  Best Local Similarity   39.1%;  Pred. No. 8.9e-30;
  Matches  120;  Conservative   67;  Mismatches  106;  Indels   14;  Gaps    5;

Qy      17 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNV 76
           | || |:|  |  | |:|||: ||| |||:  :       :| :  |: :: |: | |:
Db     302 EALGGGKFGAVCTCTERSTGLKLAAKVIKKQTPK------DKEMVLLEIEVMNQLNHRNL 355

Qy      77 ITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLHTKKI 135
           | |:   |   :::  :| : |||||: :  ::  |:| :   |::|| ||: ::|  ::
Db     356 IQLYSAIETSHEIILFMEYIEGGELFERIVDEDYQLTEVDTMVFVRQICDGILFMHKMRV 415

Qy     136 AHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLG 195
            | |||||||: ::    :  :|:||||||       : |  |||||::||:|||: :
Db     416 LHLDLKPENILCVNTTGHL--VKIIDFGLARRYNPNEKLKVNFGTPEFLSPEVVNYDQIS 473

Qy     196 LEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKL 255
            : ||||:|||||:|||| ||||||   ||| |: | :: |||| |   |: ||||:  |
Db     474 DKTDMWSLGVITYMLLSGLSPFLGDDDTETLNNVLSANWYFDEETFEAVSDEAKDFVSNL 533

Qy     256 LVKETRKRLTIQEALRHPWITPVDNQQAMVRR--ESVVNLENFRKQYVRRRWKLSFSIVS 313
           : |:   |:: :: | |||:  :  :     | :| : |   :|  ::|||| :|  ||
Db     534 ITKDQSARMSAEQCLAHPWLNNLAEKAKRCNRRLKSQILL---KKYLMKRRWKKNFIAVS 590

Qy     314 LCNHLTR 320
             |   :
Db     591 AANRFKK 597
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RESULT  12
KMLC_DICDI
ID   KMLC_DICDI     STANDARD;      PRT;   295 AA.
AC   P25323;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Myosin light chain kinase (EC 2.7.1.117) (MLCK).
GN   MLKA.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AX3;
RX   MEDLINE=91340753; PubMed=1651931;
RA   Tan J.L., Spudich J.A.;
```

```
RT   "Characterization and bacterial expression of the Dictyostelium
RT   myosin light chain kinase cDNA. Identification of an autoinhibitory
RT   domain.";
RL   J. Biol. Chem. 266:16044-16049(1991).
RN   [2]
RP   REVISIONS.
RA   Spudich J.A.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   PARTIAL SEQUENCE.
RC   STRAIN=AX3;
RX   MEDLINE=90337997; PubMed=2380188;
RA   Tan J.L., Spudich J.A.;
RT   "Dictyostelium myosin light chain kinase. Purification and
RT   characterization.";
RL   J. Biol. Chem. 265:13818-13824(1990).
CC   -!- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC       MYOSIN LIGHT CHAIN.
CC   -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC       light-chain] phosphate.
CC   -!- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
CC       AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
CC       DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       CAMK SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M64176; AAB06337.1; -.
DR   PIR; A40811; A40811.
DR   PIR; A37125; A37125.
DR   HSSP; Q63450; 1A06.
DR   DictyDb; DD01034; mlkA.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN        8    265       PROTEIN KINASE.
FT   DOMAIN      264    295       AUTOINHIBITORY DOMAIN.
FT   NP_BIND      14     22       ATP (BY SIMILARITY).
FT   BINDING      37     37       ATP (BY SIMILARITY).
FT   ACT_SITE    130    130       BY SIMILARITY.
SQ   SEQUENCE   295 AA;  33406 MW;  546CAEED8F6ECD0B CRC64;


  Query Match             29.6%;  Score 545.5;  DB 1;  Length 295;
  Best Local Similarity   40.1%;  Pred. No. 1.3e-26;
  Matches  123;  Conservative   50;  Mismatches  119;  Indels   15;  Gaps    5;

Qy       8 KVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREE-IEREVS 66
           :||  |:  |||| | |:||     | |   || | | |     |  |   |: :: ||
Db       3 EVEKIYEFKEELGRGAFSIVYLGENKQTKQRYAIKVINK-----SELGKDYEKNLKMEVD 57

Qy      67 ILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDG 126
           ||::| | |:| | ::::    :  ::|||:|||||| : :| | || :| : :|:|:
Db      58 ILKKVNHPNIIALKELFDTPEKLYLVMELVTGGELFDKIVEKGSYSEADAANLVKKIVSA 117

Qy     127 VNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAP 186
           | |||   | | ||||||::|  |   :  : : ||||:  |   :  :   ||| :|||
Db     118 VGYLHGLNIVHRDLKPENLLLKSKENHL-EVAIADFGLSKIIGQTLVMQTACGTPSYVAP 176

Qy     187 EIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSE 246
           |::|      | |||||||||||| |  || |||  |    |   :|:| ||::   |:
Db     177 EVLNATGYDKEVDMWSIGVITYILLCGFPPFYGDTVPEIFEQIMEANYEFPEEYWGGISK 236

Qy     247 LAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK 306
           ||||| |||| :  |||    || |||:   ::   :      | :    |:|:  | |
Db     237 EAKDFIGKLLVVDVSKRLNATNALNHPWLKSNNSNNTI----DTVKM----KEYIVERQK 288

Qy     307 LSFSIVS 313
           :|:
Db     289 TQTKLVN 295


RESULT  13
KCC4_RAT
ID   KCC4_RAT       STANDARD;      PRT;   474 AA.
AC   P13234;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE   (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV) [Contains: Calspermin].
GN   CAMK4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=91288548; PubMed=1648230;
RA   Ohmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT   "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RT   kinase Gr and calspermin: a gene within a gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91304387; PubMed=1649385;
RA   Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
RA   Slaughter G.R., Ono T.;
RT   "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT   cell-specific calmodulin-binding protein are derived from the same
RT   gene.";
RL   Mol. Cell. Biol. 11:3960-3971(1991).
RN   [3]
RP   SEQUENCE OF 250-474 FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX   MEDLINE=89174647; PubMed=2538431;
RA   Ohmstede C.-A., Jenson K.F., Sahyoun N.;
RT   "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT   granule cells. Identification of a novel neuronal
RT   calmodulin-dependent protein kinase.";
RL   J. Biol. Chem. 264:5866-5875(1989).
RN   [4]
RP   SEQUENCE OF 306-474 FROM N.A., AND SEQUENCE OF 335-361.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=89123272; PubMed=2914893;
RA   Ono T., Slaughter G.R., Cook R.G., Means A.R.;
RT   "Molecular cloning sequence and distribution of rat calspermin, a
RT   high affinity calmodulin-binding protein.";
RL   J. Biol. Chem. 264:2081-2087(1989).
CC   -!- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC       ENRICHED IN CEREBELLAR GRANULE CELLS.
CC   -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC       PROTEIN.
CC   -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC   -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC       TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
CC       TESTIS AND BRAIN.
CC   -!- PTM: THE N-TERMINAL OF CALSPERMIN IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       CAMK SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M63334; AAA40865.1; -.
DR   EMBL; M74488; AAA40845.1; ALT_SEQ.
DR   EMBL; M64757; AAA40856.1; -.
DR   EMBL; M64757; AAA40857.1; -.
DR   EMBL; J04600; AAA41867.1; -.
DR   EMBL; J04446; AAA40990.1; -.
DR   PIR; A41103; TVRTC4.
DR   HSSP; P00518; 1PHK.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Calmodulin-binding; Testis; Alternative splicing.
FT   CHAIN       306    474       CALSPERMIN.
FT   DOMAIN       42    296       PROTEIN KINASE.
FT   NP_BIND      48     56       ATP (BY SIMILARITY).
FT   BINDING      71     71       ATP (BY SIMILARITY).
FT   ACT_SITE    160    160       BY SIMILARITY.
FT   DOMAIN      318    337       CALMODULIN-BINDING (POTENTIAL).
FT   DOMAIN      393    399       POLY-GLU.
FT   DOMAIN      403    413       POLY-GLU.
FT   CONFLICT    372    372       I -> M (IN REF. 2 AND 4).
SQ   SEQUENCE   474 AA;  53133 MW;  56F71AC5644DED23 CRC64;
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  Query Match             28.8%;  Score 532;  DB 1;  Length 474;
  Best Local Similarity   36.8%;  Pred. No. 1.5e-25;
  Matches  119;  Conservative   62;  Mismatches  112;  Indels   30;  Gaps    7;

Qy       5 KQQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIERE 64
           |:  : ||:::  ||| |  :|| :|::| |   || | :||          | :: :  |
Db      34 KRDPLSDFFEVESELGRGATSIVYRCKQKGTQKPYALKVLKKT--------VDKKIVRTE 85

Qy      65 VSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQIL 124
             : :| :: | |:| | :::|  |::  :||||:|||||| : :|   || :|   :||||
Db      86 IGVLLRLSHPNIIKLKEIFETPTEISLVLELVTGGELFDRIVEKGYYSERDAADAVKQIL 145

Qy     125 DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPH--IKLIDFGLAHEIEDGVEFKNIFGTPE 182
             : | |||   | | |||||::      | |   :|: ||||:  :|  |  | : |||
Db     146 EAVAYLHENGIVHRDLKPENLLYA---TPAPDAPLKIADFGLSKIVEHQVLMKTVCGTPG 202

Qy     183 FVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFL---GDTKQETLANITSVSYDFDEE 239
             : ||||:     | | ||||:|:|||||| |  ||    ||  |      | :  | |
Db     203 YCAPEILRGCAYGPEVDMWSVGIITYILLCGFEPFYDERGD--QFMFRRILNCEYYFISP 260

Qy     240 FFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQ 299
             ::   |  ||| ::||:| : :||||  :||:|||:|         :  : |:::  :|:
Db     261 WWDEVSLNAKDLVKKLIVLDPKKRLTTFQALQHPWVTG--------KAANFVHMDTAQKK 312

Qy     300 Y----VRRRWKLSFSIVSLCNHL 318
                ||: | :   |   : |
Db     313 LQEFNARRKLKAAVKAVVASSRL 335
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RESULT  14
KCC1_HUMAN
ID   KCC1_HUMAN      STANDARD;      PRT;   370 AA.
AC   Q14012;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE   (CAM kinase I).
GN   CAMK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95369239; PubMed=7641687;
RA   Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
RA   Edelman A.M., Snyderman R., Means A.R.;
RT   "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT   domain structure and activation by phosphorylation at threonine-177
RT   by calcium-calmodulin dependent protein kinase I kinase.";
RL   EMBO J. 14:3679-3686(1995).
CC   -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC   -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC   -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC       PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC   -!- SUBUNIT: MONOMER.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       CAMK SUBFAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L41816; AAA99458.1; -.
DR   HSSP; Q63450; 1A06.
DR   MIM; 604998; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   Phosphorylation; ATP-binding; Alternative splicing.
FT   DOMAIN       20    276       PROTEIN KINASE.
FT   DOMAIN      287    321       CALMODULIN-BINDING (BY SIMILARITY).
FT   NP_BIND      26     34       ATP (BY SIMILARITY).
FT   BINDING      49     49       ATP.
FT   ACT_SITE    141    141       BY SIMILARITY.
FT   MOD_RES     177    177       PHOSPHORYLATION (AUTO-).
FT   MUTAGEN      49     49       K->A: LOSS OF ACTIVITY.
SQ   SEQUENCE   370 AA;  41337 MW;  57FA20ECE00FA76C CRC64;
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  Query Match             28.7%;  Score 530.5;  DB 1;  Length 370;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-25;
  Matches  120;  Conservative   65;  Mismatches  126;  Indels   25;  Gaps    9;

Qy       4 FKQ-QKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIE 62
           :|| : : | ||  : ||:| |: |    :| |     | | | | ::   : |     :|
Db      10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAK-EALEGKEG----SME 64

Qy      63 REVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQ 122
             |:::| :: | |:: | |:||:   :  |::|||||||||| : :|   :| :|:  | |
Db      65 NEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQ 124

Qy     123 ILDGVNYLHTKKIAHFDLKPENIML--LDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT 180
             :|| | |||   | | ||||||::   ||::     | : ||||:   : |       ||
Db     125 VLDAVKYLHDLGIVHRDLKPENLLYYSLDED---SKIMISDFGLSKMEDPGSVLSTACGT 181

Qy     181 PEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEF 240
             | :|||||::  :|     | |||||| |||| |  ||  :   :    |    |:||  :
```

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Db    182 PGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPY 241

Qy    241 FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWI---TPVDNQQAMVRRESVVNLENFR 297
          :   |: |||||| |: |:  || | ::||:|||    | :|        :||   |  :
Db    242 WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKN----IHQSV--SEQIK 295

Qy    298 KQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDED 333
          | : : :|| :|:  ::  |     |:|: |   ::
Db    296 KNFAKSKWKQAFNATAVVRH-----MRKLQLGTSQE 326


RESULT  15
KCC1_RAT
ID   KCC1_RAT       STANDARD;      PRT;   374 AA.
AC   Q63450; Q63084;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE   (CAM kinase I).
GN   CAMK1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (37 KDA ISOFORM).
RX   MEDLINE=94075341; PubMed=8253780;
RA   Picciotto M.R., Czernik A.J., Nairn A.C.;
RT   "Calcium/calmodulin-dependent protein kinase I. cDNA cloning and
RT   identification of autophosphorylation site.";
RL   J. Biol. Chem. 268:26512-26521(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (42 KDA ISOFORM).
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
RX   MEDLINE=95035115; PubMed=7948038;
RA   Cho F.S., Phillips K.S., Bogucki B., Weaver T.E.;
RT   "Characterization of a rat cDNA clone encoding calcium/calmodulin-
RT   dependent protein kinase I.";
RL   Biochim. Biophys. Acta 1224:156-160(1994).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM.
RC   TISSUE=Brain;
RX   MEDLINE=96182648; PubMed=8601311;
RA   Goldberg J., Nairn A.C., Kuriyan J.;
RT   "Structural basis for the autoinhibition of
RT   calcium/calmodulin-dependent protein kinase I.";
RL   Cell 84:875-887(1996).
CC   -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC   -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC   -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
CC       PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       CAMK SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L24907; AAA19670.1; -.
DR   EMBL; L26288; AAA66944.1; -.
DR   PDB; 1A06; 08-APR-98.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW   Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.
FT   DOMAIN       20    276       PROTEIN KINASE.
FT   DOMAIN      287    321       CALMODULIN-BINDING (BY SIMILARITY).
FT   NP_BIND      26     34       ATP (BY SIMILARITY).
FT   BINDING      49     49       ATP (BY SIMILARITY).
FT   ACT_SITE    141    141       BY SIMILARITY.
FT   MOD_RES     177    177       PHOSPHORYLATION (AUTO-).
FT   VARSPLIC    323    374       TSQEGQGQTASHGELLTPTAGGPAAGCCCRDCCVEPGSELP
FT                                PAPPPSSRAMD -> HQPGGTGTDS (IN 37 KDA
FT                                ISOFORM).
FT   CONFLICT    112    112       F -> G (IN REF. 1).
FT   CONFLICT    118    118       A -> R (IN REF. 1).
FT   CONFLICT    309    309       A -> R (IN REF. 1).
SQ   SEQUENCE   374 AA;  41638 MW;  37889B3DEF033AB2 CRC64;


  Query Match             28.7%;  Score 530.5;  DB 1;  Length 374;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-25;
  Matches  120;  Conservative   65;  Mismatches  126;  Indels   25;  Gaps    9;

Qy      4 FKQ-QKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIE 62
          :|| : : | ||  : ||:| |: |    :| |    | | | |: :   : |     :|
Db     10 WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKK-ALEGKEG----SME 64

Qy     63 REVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQ 122
            |:::| :: | |:: | |:||:   :  |::|||||||| : :|   :| :|:  | |
Db     65 NEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQ 124

Qy    123 ILDGVNYLHTKKIAHFDLKPENIML--LDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT 180
          :|| | |||   | | ||||||::   ||::     | : ||||:   : |       ||
Db    125 VLDAVKYLHDLGIVHRDLKPENLLYYSLDED---SKIMISDFGLSKMEDPGSVLSTACGT 181

Qy    181 PEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEF 240
          | :||||::  :|     | |||||| |||| |  ||  :   :    |    |:||  :
Db    182 PGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPY 241

Qy    241 FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWI---TPVDNQQAMVRRESVVNLENFR 297
          :   |: |||||| |: |:  || | ::||:|||    | :|        :||   |  :
Db    242 WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKN----IHQSV--SEQIK 295

Qy    298 KQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDED 333
          | : : :|| :|:  ::  |     |:|: |   ::
Db    296 KNFAKSKWKQAFNATAVVRH-----MRKLQLGTSQE 326


Search completed: May 18, 2002, 05:12:35
Job time: 1436 sec
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